#6

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May 15, 2017

R. Paul Frasier
District Attorney for Coos County
Office of the District Attorney
Coos County Courthouse
250 N. Baxter Street
Coquille, OR 97423

Re: McGuffin v. Nooth 15CV1030

Dear Mr. Frasier,

I have reviewed Oregon State Police Forensic Laboratory reports dated August 27, 2000, September 6, 2000, November 3, 2000, December 9, 2001, January 21, 2002, and April 17, 2002, as well as notes and other records from which the reports were prepared. I have also reviewed a letter with attached spreadsheets addressed to Oregon Department of Justice dated March 6, 2017, Oregon State Police meeting "Lab Notes" dated April 24, 2017, and an OSP Laboratory report dated May 9, 2017.

Lastly, I have reviewed OSP Laboratory's STR Casework Protocols dated August 1, 2000, October 11, 2000, April 9, 2001, February 22, 2010, and October 7, 2010. It should be noted that the 2010 protocols pertain to particular STR methods that were not available in 2000 and 2001, but later supplanted the methods in use at that earlier time.

The Right Shoe, Exhibit 1

I understand from these materials that, within days of the June 28, 2000, disappearance of Coquille High School student Leah Freeman, a right shoe was found in a public road. No bloodstain appears to have been present on it, but two cuttings of the shoe taken and analyzed by OSP (as samples **1.1** and **1.3**) each showed a mixture of DNA from (likely) two persons. The major portion of each mixture matches the DNA profile of Leah Freeman. The minor portion of sample **1.3** arose from a male person. The minor portion of sample **1.1** arose from someone else, but the gender of its source cannot be discerned from the test results. A third shoe cutting (sample **1.2**) gave no results.

6-1

The OSP laboratory's report of these results, dated August 27, 2000, is scandalously incomplete. Regarding Exhibit 1, the analyst reported only that "The DNA profile (sic) … matches the DNA profile from Leah Freeman." No DNA mixtures on the shoe were mentioned; in particular, the finding of male DNA on the shoe was withheld.

It should be noted that these omissions were not sanctioned by the STR Casework Protocols in place at the time of the report. The DNA Interpretation Guidelines dated August 1, 2000, (at page 31, attached as Appendix 1) instruct OSP analysts how to recognize DNA mixtures, how to estimate an approximate number of mixture contributors, and how to distinguish major from minor mixture contributors (in cases where the relative amounts of individual DNA contribution may be substantially different between contributors).

Appropriately, the analyst's notes (excerpted in Figure 1, below) do correctly summarize the test results from each mixture in a manner that unambiguously identifies the major and minor DNA contributions to each one. Results at the Amelogenin locus (abbreviated Amel.) for sample **1.3** indicate the detection of Y-chromosome from a male person as a minor contributor to the mixture. The complete note is attached as Appendix 2.

Right Shoe DNA Mixtures

Analyst: MHC

Profiler Plus Genotype Summary of Results

Date: 07~~27~~31 MHC RUN: 072600

CDL/Ex.	D3S1358	vWA	FGA	Amel.	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820
IN).3 9947A CONTROL	14,15	17,18	23,24	X,X	13,13	30,30	15,19	11,11	11,11	10,11
IN).6 OON-481#1.1	14,17>(16)	17,18>(16)	23,25>(6)	X,X	10,13	28,31.2> (30)	12,16	11,13>(12)	10,11	11,12
IN).7 OON-481#1.2				NO ALLELES DETECTED						
IN).8 OON-481#1.3	14,17> (15,16)	17,18> (16,20)	23,25> (19)	X>(Y)	10,13> (11,12)	28,31.2> (25,31)	12,16	11,13> 12	10,11> (8,12)	11,12> (8,10)
IN).16 OON-481#2.2				NO ALLELES DETECTED						

Figure 1

At pages 41 and 42 of the STR Casework Protocols (attached as Appendix 3), Report Writing Guidelines indicate how DNA mixtures are to be reported. These guidelines, however, were obviously ignored.

It should be noted that the terms of ASCLD-LAB accreditation (held by the OSP laboratory in 2000) required a technical review of the casefile by a second qualified analyst prior to publishing any report. Competent technical review would doubtless have improved the August, 27, 2000, OSP report. The records I have reviewed, however, contain no documentation of technical review having been undertaken. Further, no

6-2

technical review procedure is specified in the STR Casework Protocols dated August 1, 2000.

The Left Shoe, Exhibit 2

I also understand from the materials I reviewed that, on July 4, 2000, Sheriff's Deputy Kip Oswald found a left shoe in a dirt road about fifteen miles from Coquille. Bloodstaining on the shoe sole was recovered by OSP to six swabs. Two of them were tested, as were three cuttings from apparently unstained areas of the shoe. The blood samples (**2.1.2** and **2.1.4**) were observed to have the same DNA profile as Leah Freeman. DNA mixtures from (likely) two persons were obtained from two of the shoe cuttings (**2.3** and **2.4**), whereas the third cutting (sample **2.2**) gave no results. The major portion of each mixture has the same DNA profile as Leah Freeman, whereas the minor portions each arose from a male person who is possibly the same male in each sample.

The test results were reported by OSP in the same August 27, 2000, laboratory report as the right shoe (Ex. 1) results discussed above. Curiously, the minor male component on the left shoe (sample **2.3**) was correctly reported, in contrast to the slipshod account of the right shoe. The test results from the sample **2.4** mixture were omitted from mention, however, in a similarly deficient manner.

Left Shoe DNA Mixtures

Analyst: [illegible] Profiler Plus Genotype Summary of Results Date: 073100 Rvd: 072600

COL/Ex.	D3S1358	vWA	FGA	Amel.	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820
INJ.43 CON-481#2.3	14,17>16> (15)	17,18	23>25> (19,24)	X>Y	10,13	28,31.2> (29,30)	12,16	11,13> 12>(10)	10,11> (12,14)	11>12> (7,10)
INJ.44 CON-481#2.1.4	14,17	17,18	23,25	X,X	10,13	28,31.2	(12)	11,13	(10,11)	(11,12)
INJ.51 CON-481#2.1	14,17> (9.3)	17,18	23,25	0,5 X>Y	10,13> 12>(6)	28,31.2> (29)	(12,16)	11,13> (12)	10,11	(11,12)
Rvd: 080200										

Figure 2

As with the right shoe, the analyst's notes (further excerpted in Figure 2, above) summarize the test results from each left shoe mixture in a manner that identifies the major and minor DNA contributions to each one. Results at the Amelogenin locus for samples **2.3** and **2.4** indicate the detection of Y-chromosome from a male person. The complete note is attached as Appendix 2. It may be noted that the summary has been re-assessed in the April, 2017, OSP meeting "Lab Notes". Allele 10 at locus D5S818 in sample **2.3** is apparently now considered to be a "stutter" artifact; it was omitted from the compilation of test results in the "Notes".

6-3

On January 21, 2002, Oswald's DNA profile was reported by OSP laboratory to be "consistent with" the minor contributor to the mixture. On May 9, 2017, however, Oswald and others (including McGuffin) were reported by a different OSP analyst to be excluded as the source of this DNA. I agree with the more recent report: Oswald is not the male on the left shoe. I also agree with the recent OSP conclusion that Oswald, McGuffin and others are not the (previously undisclosed) male on the right shoe.

The results for the shoe sample **2.3** at locus D13S317 indicate that the minor male contributor possess alleles 12 and 14. Oswald, however, has alleles 11 and 12 at this locus (see Figure 3, below). He has no allele 14. By simple inspection, consequently, he is excluded as the minor male on the shoe. (Whether or not allele 10 at D5S818 is actually "stutter" artifact is not germane to the exclusion, given Oswald's 10,12 at this locus.) In my view, the exclusion would have been obvious to any competent DNA analyst in 2002.

Oswald's DNA profile from sample **47** is shown on the last line in Figure 3, below.

Deputy Kip Oswald's DNA Profile (#47)

Run Date: 011602 Analyst: Mike O Date: 011702

CDL No./Ex No.	D3S1358	vWA	FGA	Am	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820
PP LADDER	12-19	11-21	18-30	X,Y	8-19	24.2-36.38	9-26	7-16	8-15	6-15
9947A Control	14,15	17,18	23,24	X,X	13,13	30,30	15,19	11,11	11,11	10,11
PCR Control			NO ALLELES							
011702 Reinjection										
PP LADDER	12-19	11-21	18-30	X,Y	8-19	24.2-36.38	9-26	7-16	8-15	6-15
OON-481 #47	16,16	17,18	19,24	X,Y	13,13	29,30	13,20	10,12	11,12	7,10

Figure 3

In STR Casework Protocols dated April 9, 2001, (at pages 57 and 58, attached in Appendix 4) Report Writing Guidelines instruct OSP analysts how to recognize and report exclusions. Moreover, and in contrast to the 2000 protocols which omitted it, a requirement for technical review is specified on page 59. The records I have reviewed, however, contain no documentation of technical review having been undertaken. Clearly, an opportunity to avoid the erroneous attribution to Oswald was missed in 2002.

6-4

Recommendations

The male contributors of the DNA recovered from the right and left shoes are unidentified at present. Moreover, the test results describing their DNA profiles are apparently unsuitable for entry into the OSP DNA database "due to low levels of DNA". Indeed, their DNA profiles are incomplete and, consequently, ambiguous; some of their alleles may not have been detected due to their low preponderance compared with the much larger amount of DNA from Leah Freeman. Of course, if either man is not represented in the database, then he can only be compared to the shoes by testing him directly.

It may be noted there can be no guarantee that the male DNA on the shoes is attributable to Leah Freeman's assailant(s), since it may have been deposited during some non-sinister event(s) before or after she was assaulted. Nevertheless, the possible involvement of these men might be thought to require investigation that was precluded by OSP laboratory errors.

DNA from the shoe mixtures should be re-tested in an attempt to identify the male profiles unambiguously. This should be attempted in each of two ways:

1. DNA remaining at OSP from the preparation of shoe samples **1.3** and **2.4** in 2000 should be re-amplified. Additional genetic information about the male DNA may be expected from this work due to increased sensitivity and other improvements in DNA analysis in the years since 2000. The amount of extracted DNA that remained from these two stains after the analysis in 2000 is documented in the lab notes to be ample for retesting, whereas all the other shoe extracts were apparently consumed.

It should be noted that sample **1.3** is the evidence for an unknown male on the right shoe that was unreported until recently. Sample **2.4**, from the left shoe, previously provided very little genetic information compared with sample 2.3 (which was erroneously attributed to Deputy Oswald until recently), but it does contain male DNA; he may be the same male as detected in sample 2.3 (which was consumed). Moreover, it may be noted that the amplification of sample **2.4** at OSP was defective; numerous biochemical artifacts of the PCR amplification process are apparent in the test results for this sample. In my view, it should have been re-amplified at the time.

2. Since it is unknown whether any improvement in the male profiles resulting from re-amplification of the original DNA samples would qualify them for entry to the database, the right and left shoes should be re-examined for male DNA that may yet remain on them. The results of re-examination can be agreed in advance, if they are successful, to qualify for database upload and search.

3. A number of recommendations for additional testing were advanced in a letter by Oregon Innocence Project to Oregon Department of Justice dated March 6, 2017. I do not agree that the various additional tests suggested therein can be useful at present.

3a. Ms. Freeman's clothing, discussed in the letter at page 6 of 9, was previously tested at OSP, the UK Forensic Science Service (when attempted DNA testing was unsuccessful and no semen or useful bloodstains were apparently detected), and later at Microtrace, Inc. (where no DNA testing was attempted). The letter suggests that DNA deposited by the perpetrator, who may have "handled or touched the clothing", may yet be recovered. As with the shoes, however, there can be no guarantee that any DNA recovered from the clothing is attributable to Leah Freeman's assailant(s), especially given the history of handling and touching that has occurred since 2000.

3b. The letter also proposes that hairs recovered from the clothing be tested for mitochondrial DNA (mtDNA) to confirm or refute whether they are Leah Freeman's own hairs. It is unclear to me how this could be helpful. The relevance of any hair must be doubtful. Should any hair demonstrate her own mtDNA sequence, one still could not know whether the hair originated from the victim, from someone else who has the same sequence by coincidence, or from a maternal relative. Nor would it be helpful to identify a hair with a non-Freeman sequence, because there is no mtDNA database of offenders to interrogate with it. Moreover, since mtDNA results are not capable of comparison to STR results, it will not be possible to determine whether any non-Freeman hair came from either of the unidentified men on the shoes. Any candidate source can only be compared to a hair by testing him (or a maternal relative) directly.

3c. The letter proposes to test cellophane found beneath the victim's head. Its presence at the scene may be coincidental, and it may be expected to be heavily loaded with victim's DNA. STR testing is unlikely, in my view, to be helpful.

3d. Other testing, including Y-STRs, is proposed for some later stage. It should be noted that Y-STR testing, as an investigative tool, suffers from the same handicaps as mtDNA testing. There is no Y-STR database of offenders to interrogate. Moreover, it will not be possible to determine whether any Y-STR profile came from either of the unidentified men on the shoes, since Y-STR results are not capable of comparison to autosomal (i.e., "regular") STRs.

I hope these remarks are helpful. Please let me know if you have any questions.

Sincerely,

Thomas Fedor
Forensic Serology and DNA Consultant

6-6

Appendix 1

OSP STR Casework Protocols dated August 1, 2000

At page 31, DNA Interpretation Guidelines

6-7

Evaluation of STR Data (cont.)

loci in question, the number of loci affected and the percent disparity between alleles, the sample may need to be re-amplified and re-run.

- Other causes of imbalance at a locus include degraded DNA, presence of inhibitors, extremely low amounts of input DNA, or primer mis-match.

6. Mixtures may be indicated by the following:

   a. The presence of more than two alleles per locus at more than one locus

   b. The presence of a peak at a stutter position that is greater in peak height than that typically observed for stutter in a single source sample

   c. Significantly imbalanced alleles for a heterozygous genotype at more than one locus.

In some cases it may be possible to estimate the approximate number of contributors by considering number of alleles present at a locus, the appearance of the allelic patterns within and between loci, etc.

In some DNA mixtures a minor contributor and/or a major contributor may be distinguishable, especially when there is a significant difference in amounts of input DNA from the different contributors.

When a contributor is known or expected to be present, as in certain sexual assault samples where the victim's epithelial cells have been incompletely separated from the sperm cells, assignment of the known contributor's alleles may allow for determination of the remaining profile.

In other DNA mixtures, the donors of the individual peaks may be unclear. Under these circumstances, it may be reported that a given individual can or cannot be excluded as a contributor to the mixture.

The likelihood that any sample is a mixture must be determined by the analyst by assessing all of the DNA case information including the information provided by the known reference standards.

DNA typing results at other loci (e.g. DQA1, PM, D1S80, RFLP, etc.) may also be considered in interpreting mixtures.

6-8

Appendix 2

OSP Laboratory Notes

Documenting DNA Mixtures with
Minor Male Contributors on Right and Left Shoes

6-9

Analyst: MHC

Profiler Plus Genotype Summary of Results

Date: 07~~27~~31 MHC RUN: 072600

CDL/Ex.	D3S1358	vWA	FGA	Amel.	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820
INJ.3 9947A CONTROL	14,15	17,18	23,24	X,X	13,13	30,30	15,19	11,11	11,11	10,11
INJ.6 OON-481#1.1	14,17>(16)	17,18>(16)	23,25>(24)	X,X	10,13	28,31.2> (30)	12,16	11,13>(12)	10,11	11,12
INJ.7 OON-481#1.2	—	—	—	NO ALLELES DETECTED				—	—	—
INJ.8 OON-481#1.3	14,17> (15,16)	17,18> (16,20)	23,25> (19)	X>(Y)	10,13> (11,12)	28,31.2> (29,31)	12,16	11,13> 12	10,11> (8,12)	11,12> (8,10)
INJ.10 OON-481#2.2	—	—	—	NO ALLELES DETECTED				—	—	—
INJ.12 OON-481#2.1.2	14,17	17,18	23.25	X,X	10,13	28,31.2	12,16	11,13	10,11	11,12
INJ.14 RB072400#2	—	—	—	NO ALLELES DETECTED				—	—	—
INJ.16 RB072300	—	—	—	NO ALLELES DETECTED				—	—	—
INJ.33 OON-481#4	14,17	17,18	23.25	X,X	10,13	28,31.2	12,16	11,13	10,11	11,12
INJ.34 RB072400#3	—	—	—	NO ALLELES DETECTED				—	—	—

Key: > = greater than; < = less than; ( ) = 50-150 RFUs

1337 151 MHC

DistrictAttorney_000049

Exhibit 75, Page 10 of 21

Profiler Plus Genotype Summary of Results

Analyst: MAHL Date: 073100 Run: 0726 QC

CDL/Ex.	D3S1358	vWA	FGA	Amel.	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820
INJ.43	14,17>16> (15)	17,18	23>25> (19,24)	X>Y	10,13	28,31.2> (25,30)	12,16	11,13> 12>(10)	10,11> (12,14)	11>12> (7,10)
QON-481 #23										
INJ.44	14,17	17,18	23,25	X,X	10,13	28,31.2	(12)	11,13	(10,11)	(11,12)
QON-481 #2.1.4										
INJ.51	14,17> (16.2)	17,18	23,25	0.5 X>Y	10,13> 12>(6)	28,31.2> (25)	(12,16)	11,13> (12)	10,11	(11,12)
QON-481 #2.4										
Run: 080200										
INJ.17										
PCR Control										

No Alleles Detected

Key: > = greater than; < = less than; ( ) = 50-150 RFUs

DistrictAttorney_000050

Appendix 3

OSP STR Casework Protocols dated August 1, 2000

At pages 41 and 42, Report Writing Guidelines

6-12

STR Analysis for Casework
Oregon State Police DNA Unit

Report Writing Guidelines (cont.)

Results/Conclusions:

Inclusions

1. Single Source Stains

   If, at a particular locus, each allelic peak above 150 RFU in the evidence sample is observed in the reference standard:

   - "The STR profile from Exhibit X (description) matches that from Individual A at all 13 loci (or a subset thereof). The frequency of occurrence of an unrelated individual in a random population exhibiting the STR profile observed in Exhibit X is 1 in xxxx Caucasians and 1 in xxxx African-Americans.

   If the match was based on a partial profile (i.e. there are allelic peaks consistent with Individual A but they are below 150 RFU at one or more loci), an additional statement may be included:

   - "The results at the remaining loci were inconclusive/below the threshold for making a conclusive determination of the contributor; however, Individual A is not excluded as a possible donor at these loci."

2. Mixed Stains

   If a DNA mixture is indicated by the presence of three or more allelic peaks and/or peak balance <70% at multiple loci:

   - "The STR typing results from Exhibit X (description) indicate the presence of a DNA mixture, i.e. DNA from more than one contributor."

   If the allelic peaks are consistent with two donors and a major profile matching that of Individual A can be clearly discerned:

   - "The major profile matches that from individual A. This frequency of occurrence..."

Report Writing Guidelines (cont.)

If allelic peaks from a minor contributor are present that are consistent with coming from Individual B:

- "The minor profile matches that of Individual B. This frequency of occurrence...."

If there are multiple minor contributors:

- "Individuals B and C cannot be excluded as minor contributors."

If a mixture is identified, but differences in allelic peak height are not large enough to discern a major and minor type:

- "Neither Individual A nor Individual B can be excluded as a contributor to the mixture" or "The mixture is consistent with a mixture of DNA from individuals A and B."

  Note: In general, no frequency will be reported in these situations. On a case-by-case basis, a P_E (probability of exclusion) may be calculated.

3. It is not necessary to include a statistical interpretation for results that are non-probative.

Exclusions

If allelic peaks in the profile from a reference standard are not found in the profile derived from the evidence sample, and their absence cannot be attributed to insufficient template, degradation, inhibition, or masking at a stutter position:

- "The STR profile of Exhibit A (description) does not match that of Individual A. Therefore, Individual A is excluded as a possible donor."

Or for a mixed stain:

- "Individual A can be excluded as a contributor to the mixture."

6-14

Appendix 4

OSP STR Casework Protocols dated April 9, 2001

At pages 57 and 58, Report Writing Guidelines
Re : Exclusions

And

At page 59, Technical Peer Review

6-15

DistrictAttorney_000054

"The major STR profile from Exhibit X (description) is consistent with coming from Individual A. The frequency of occurrence of an unrelated individual in a random population exhibiting the STR profile observed in Exhibit X is 1 in xxxx in Caucasians, 1 in xxxx in Hispanics and 1 in xxxx inAfrican-Americans."

If allelic peaks from a minor contributor are present that are consistent with coming from Individual B and the statistical frequencies are less than 1 in 10 billion:

- "The minor profile matches that of Individual B. This frequency of occurrence…."

If allelic peaks from a minor contributor are present that are consistent with coming from Individual B and the statistical frequencies are greater than 1 in 10 billion:

"The minor profile is consistent with coming from of Individual B. The frequency of occurrence of an unrelated individual in a random population exhibiting the STR profile observed in Exhibit X is 1 in xxxx Caucasians, 1 in xxxx Hispanics and 1 in xxxx African-Americans."

If there are multiple minor contributors:

- "Individuals B and C cannot be excluded as minor contributors."

If a mixture is identified, but differences in allelic peak height are not large enough to discern a major and minor type:

- "Neither Individual A nor Individual B can be excluded as a contributor to the mixture" or "The mixture is consistent with a mixture of DNA from individuals A and B."

  Note: On a case-by-case basis, a P_E (probability of exclusion) may be calculated.

3. It is not necessary to include a statistical interpretation for results that are non-probative.

Exclusions

If allelic peaks in the profile from a reference standard are not found in the profile derived from the evidence sample, and their absence cannot be attributed to insufficient template, degradation, inhibition, or masking at a stutter position:

- "The STR profile of Exhibit A (description) does not match that of Individual A. Therefore, Individual A is excluded as a possible donor."

Or for a mixed stain:

- "Individual A can be excluded as a contributor to the mixture."

Note: Peaks between 50 and 150 RFU will be considered for purposes of exclusion

Inconclusive Results

If no allelic peaks above the threshold are present, yet there are peaks between 50 and 150 RFU:

- "No STR profile of Exhibit X (description) could be conclusively determined due to …(e.g. insufficient and/or degraded DNA)."

No Result

"No result" is reported if no allelic peaks greater than 50 RFU are observed. No result may be obtained at all or some loci, depending upon the quantity and/or quality of the DNA.

Statistical Interpretation:

1. Allelic peaks must be greater than 150 RFU to be used to make a statistical interpretation.

2. Include in the report the database used to make the statistical interpretation.

   "The population frequencies are calculated from the allele frequencies published by the FBI in the Journal of Forensic Sciences (J. Forensic Sci. (1999) 44(6):1277-1286).

STR Analysis for Casework
Oregon State Police DNA Unit

Technical Peer Review

The report and all data contained in the case file shall be independently reviewed by a second qualified analyst to confirm that the conclusions are scientifically supported by the data and that the interpretations have been made objectively according to the laboratory's interpretation guidelines. The reviewer will incorporate the following elements in the technical review:

- Check electropherograms for the positive control and the negative controls (PCR blanks and reagent blanks)
- Check the allelic ladders.
- Check the ROX Internal Lane Size Standards for 75bp, 246bp, and 350/400bp peaks.
- Check precision using the 246bp fragment sizings.
- Check the resolution of the ladder used to genotype.
- Check accuracy of allele calls.

Note: The electronic Genescan and/or Genotyper files can be accessed if necessary.

- Ascertain that the conclusions drawn in the report are supported by the data and that the statistical interpretation follows laboratory guidelines.
- Check that all necessary documentation is present in the case file.
- Enter typing data into CODIS (if appropriate)
- Mark "Technical Review" milestone in LIMS.
- Initial and date case file.

Any differences between the two readers must be resolved prior to issuing a final interpretation and report. If, after review and discussion of the data, disagreement remains regarding a particular result or conclusion, the case file will be referred to the technical leader for a final decision.

Paul Frasier

From: Thomas Fedor [thomas.fedor@att.net]
Sent: Thursday, May 18, 2017 10:35 AM
To: Paul Frasier
Subject: Re: McGuffin Case

#7

No comments re IP's letter.

Re crime lab:

Author seems to be speculating that, simply because she considers it to have been optional, original analyst omitted **1.1** mixture because "not best result". How "best" might be evaluated is unspecified.

Hard to argue with omitting negative results from **1.2**, although one would want to include it simply to fend off questions. Widespread and sensible practice for years (elsewhere than OSP, apparently). Defense, at least, will be curious if they review the lab records pre-trial. Don't these guys ever have to testify? I see from IP that the analyst in this case did not.

Re 1.3: Speculates why minor male unreported is because all less than 150. Protocol p30 Introduction: "Every possible situation not covered." In particular, evaluation at Amelogenin not once addressed in Protocol. I do not agree that ignoring the undisclosed male would or should have been considered to be "conservative" in the context of this (or any) case. If it may be that the analyst was ignorant of context, then she can have had no basis for evaluating what is conservative.

I disagree that 2.3 minor ("Not Oswald") is "primarily above the 150 threshold", and OSP "Lab Notes" April 2017 confirm it is primarily btw. 50 - 150. Further, she speculates what data original analyst considered or not (50 - 150), as no record exists. Moreover, as IP mentions, 2001 Protocol p58 says 50 - 150 "**will** be considered for purposes of exclusion".

Justification for omitting **2.4** not attempted, but presumably "not best result". Indeed not. As I noted in my report, should have been redone at the time.

How to justify withholding conclusions from multiple sample testing? How to determine "best" result? Invites review of all 2000 testing?

Hope this helps.

Regards,

TF

On May 17, 2017, at 1:57 PM, Paul Frasier <pfrasier@co.coos.or.us> wrote:

7-1

As of today's mail I have not received your written report.

.ave received a letter from the IP giving their position and from the crime lab given me today and yesterday.

Do you have any comments?

R. Paul Frasier
District Attorney for Coos County Oregon
North Baxter
Coquille, Oregon 97423
541-396-7555

<IP and OSP reasons.pdf>

7-2

Paul Frasier

From: Thomas Fedor [thomas.fedor@att.net]
Sent: Wednesday, May 31, 2017 6:17 PM
To: Paul Frasier
Subject: Re: State v. McGuffin
Attachments: Freeman DNA Materials Part #3 excerpt.pdf; ATT00001.htm

#8

Our conversation did change my information, but not my conclusions. Indeed, perhaps I was too gentle.

The 2000 report was apparently not only technically reviewed by another analyst, it was also reviewed by the "Technical Leader". The TL is the person responsible for the entire technical operation of the DNA lab. I was offered copy documentation, it's in a different binder than the stuff I've seen. I declined, as I don't think I really need to see it.

And I do understand that Stephanie reads the protocol (p30 item 3) as possibly meaning "Alleles less than 150 RFU may be ignored." And we both agree that the protocol is badly written, as were most forensic DNA lab protocols of the era.

Nevertheless, I'm flabbergasted at the depth of bad judgment *times three* that was exhibited in the 2000 report.

I have not changed my views about the Oswald mis-attribution. The protocol seems unambiguous: Alleles btw. 50 - 150 RFU will be considered for purposes of exclusion.

Maybe the analyst continued to be negligent or incompetent. That the technical reviewer also missed the exclusion, however, is inexcusable. And they both missed the exclusion of Oswald from the previously undisclosed 1.3 mixture as well, thereby compounding disregard for protocol with original bad judgement. (And a failure to read the lab submission form requesting that Oswald be tested, see attached.)

Moreover, the reported mis-attribution disregarded *additional* bits of protocol. The report writing guidelines at pp 57 - 58 describe the language by which various orders of *non*-exclusions are to be reported. The odious phrase "consistent with" is *not* an option.

I also learned that it was *unwritten* laboratory practice (apparently throughout OSP, not just DNA) to report only the "best results" from multiple samplings of the "same" thing, whatever that means. The power point presentation you sent claims the practice was "protocol". But it wasn't anything so formal, it seems.

Hope this helps.

Regards,

TF

8-1